AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph beginning on page 1, at line 1 as follows:

METHODS FOR MICROBIAL IDENTIFICATION ~~CHIP~~ BASED ON DNA-DNA HYBRIDIZATION

Please replace the paragraph beginning on page 32, at line 5 as follows:

In this Example, the production of one microarray embodiment is described. Genomic DNAs from four fluorescent *Pseudomonas* strains (*Pseudomonas fluorescens* (ATCC 13525^T), *P. chlororaphis* (ATCC 9447), *P. putida* (ATCC 12633^T), and *P. aeruginosa* (ATCC 15692); *i.e.,* the "reference strains") were fragmented by bead-beating to ensure randomness, and the fragments were size-fractionated (1 to 2 kb) by agarose gel electrophoresis, as known in the art. The ~~QIAquick~~ QIAQUICK Gel Extraction Kit (Qiagen) was used to elute and purify DNA from the agarose gel, according to the manufacturer's instructions. The genomic DNA fragments were inserted to pPCR-Script Amp vector (Stratagene), then PCR amplified with the T3/T7 promoter primer set using standard PCR conditions, with a primer annealing temperature of 55°C. Amplified genomic DNA fragments were purified with ~~QIAquick~~ QIAQUICK 8 PCR purification kit (Qiagen) and quantified with ~~PicoGreen~~ PICOGREEN (Molecular Probes), according to the manufacturer's instructions.

Please replace the paragraph beginning on page 32, at line 18 as follows:

Purified DNAs were resuspended (200 ng/μl) in 3X SSC (1X SSC is 0.15 M NaCl, plus 0.015 M sodium citrate), and printed using approximately 1 nl/spot, on CMT-GAPS amino silane coated slides (Corning). In these experiments, 92, 90, 96, and 60 fragments from *P. fluorescens, P. chlororaphis*, *P. putida*, and *P. aeruginosa* were spotted in duplicate, respectively. Yeast gene *STE* (pheromone receptor gene; ~~GenBank~~ GENBANK accession no. M12239) was spotted as positive control, and yeast gene *ACT* (actin gene; ~~GenBank~~ GENBANK accession no. L00026), lambda DNA, and water were spotted as negative controls. PCR primer pair, STE3F1 (CCC CTT CAA AAT TGG AGC TTG C; SEQ ID NO:1) and STE3R1 (CCC CCT TTA GCA TGG CAT TCA; SEQ ID NO:2), and pair ACT1F1 (GAT GGA GCC AAA GCG GTG A (SEQ ID NO:3) and ACT1R1 (GCG CTT

GCA CCA TCC CAT T; SEQ ID NO:4) were used to amplify the *STE* and *ACT* yeast genes, respectively.

Please replace the paragraph beginning on page 33, at line 25 as follows:

In this Example, the methods used to analyze the data obtained from the hybridized arrays of one embodiment of the present invention are described. Hybridized arrays were scanned with a ~~GenePix~~ GENEPIX 4000 laser scanner (Axon). Laser lights of wavelength at 532 and 635 nm were used to excite Cy3 dye and Cy5 dyes, respectively. Fluorescent images were captured as multi-image-tagged image file format (TIFF) and analyzed with ~~GenePix~~ GENEPIX Pro 3.0 software (Axon). The ratio (*R*) of the extent of hybridization between test DNAs and reference DNAs was derived from a median value of pixel-by-pixel ratios. By using this approach to calculate *R*, non-specific signals, which appear in both wavelength images, were found to have less of an effect than when the mean values of a whole spot were used.

Please replace the paragraph beginning on page 36, at line 7 as follows:

In addition, situations in which different strains of the same species have differences in genome size (*e.g., E. coli* K12, as compared to *E. coli* O157; ~~GenBank~~ GENBANK accession nos. U00096 and AE005174, respectively) were taken into consideration. It is not contemplated that this scale of difference (1 of 5 Mb) will invalidate the methods of the present invention, although the percent similarity should be slightly higher than the average percent similarity from whole-genome DNA-DNA hybridization.